STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 4.4.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (httm, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 10/568,737									
ATTN: NEW RULES CASES:	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE									
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."									
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.									
3Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.									
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.									
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.									
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.									
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.									
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number .000									
9Use of n's of Xaa's (NEW BULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.									
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220> <223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)									
11Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules									
PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.									
13 Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>									



IFWP

RAW SEQUENCE LISTING DATE: 02/27/2006
PATENT APPLICATION: US/10/568,737 TIME: 15:06:53

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Output Set: N:\CRF4\02272006\J568737.raw

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      7 <130> FILE REFERENCE: 51564-44
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/568,737
C--> 10 <141> CURRENT FILING DATE: 2006-02-15
     12 <150> PRIOR APPLICATION NUMBER: US 60/495,094
                                                               Dres Met Cemply
     13 <151> PRIOR FILING DATE: 2003-08-15
                                                               Corrected Distrotte Needed)

(Pg. S)
     15 <160> NUMBER OF SEQ ID NOS: 44
     17 <170> SOFTWARE: PatentIn version 3.3
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     20 <211> LENGTH: 537
     21 <212> TYPE: DNA
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                    20
                                                             30
     59 Leu Thr Arg Glu Phe Asn Lys Asn Ile Glu Ile Lys Val Glu Gly Thr
                35
                                    40
     63 Glu Ile Thr Val Val Arg Pro Asn Asp Ser Lys Glu Met Lys Thr Ile
     67 His Gly Thr Thr Arg Ala Asn Leu Asn Asn Met Val Val Gly Val Ser
                                                75
                            70
     71 Glu Gly Phe Lys Lys Asp Leu Glu Met Lys Gly Val Gly Tyr Arg Ala
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                        85
     75 Gln Leu Gln Gly Thr Lys Leu Val Leu Ser Val Gly Lys Ser His Gln
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79 Asp Glu Val Glu Ala Pro Glu Gly Ile Thr Phe Thr Val Ala Asn Pro

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PATENT APPLICATION: US/10/568,737 TIME: 15:06:53

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Output Set: N:\CRF4\02272006\J568737.raw

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109 tctagtgtca acaaagtaaa agccttaacc ataaaagaag ccatggaaca aggaaaagat
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125 gctactgcca caacggaaaa aggtaaacta gagtatgaca ccgttaagtc agacaccgca
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                                40
169 Leu Thr Ile Lys Glu Ala Met Glu Gln Gly Lys Asp Ile Ser Leu Thr
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173 Leu Ala Gly Glu Val Thr Ala Asn Asn Ser Ser Lys Val Lys Ile Asp

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185 Thr Ala Gln Ser Ser Glu Phe Asp Val Gln Thr Lys Ala Asn Gln Leu
          115
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189 Gln Val Ala Lys Thr Asn Ala Ala Leu Lys Trp Glu Thr Tyr Asn Arq
      130
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193 Lys Val Asn Glu Ile Asn Thr Leu Lys Ser Arg Tyr Asn Thr Ala Pro
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197 Asp Glu Ser Leu Leu Glu Gln Ile Arg Ser Ala Glu Asp Ser Val Ser
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205 Gln Ile Glu Leu Asp Lys Ala Asn Ala Thr Ala Thr Thr Glu Lys Gly
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209 Lys Leu Glu Tyr Asp Thr Val Lys Ser Asp Thr Ala Gly Thr Ile Val
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237 Tyr Val Ile Glu Leu Asp Gln Ser Asp Lys Gln Pro Leu Ile Gly Ser
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245 Val Leu Lys Glu Thr Phe Thr Met Ala Glu Asn Gly Lys Thr Tyr Val
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DATE: 02/27/2006

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                260
                                     265
377 Lys Leu Asn Tyr Pro Glu Ala Leu Asp Thr Leu Thr Gln Leu Phe Asp
            275
                                 280
381 His Val Gly Asp His Pro
                             - Invalid hospunse
        290
382
385 <210> SEQ ID NO: 7
386 <211> LENGTH: 34
387 <212> TYPE: DNA
388 <213> ORGANISM: / Primer
390 <400> SEQUENCE: \
                               Invalid Response
391 gagaaaatac atatgtcacg tattggtaat aaag
394 <210> SEQ ID NO: 8
395 <211> LENGTH: 29
396 <212> TYPE: DNA/
397 <213> ORGANISM: Primer
399 <400> SEQUENCE:
400 ccctcgagtt atttacctgt tttaccttc
403 <210> SEQ ID NO: 9
404 <211> LENGTH: 31
406 <213 > ORGANISM: Primer S AME EVWY
408 <400 > SECTION OF
                                                                erv310n
Summany
Sheeti
408 <400> SEQUENCE: >
409 aaggatccca tgtcacgtat tggtaataaa g
412 <210> SEQ ID NO: 10
413 <211> LENGTH: 38
414 <212> TYPE: DNA/
415 <213 > ORGANISM: Primer
417 <400> SEQUENCE: 10
418 actagtcgac ttatttacct gttttacctt ctttaagg
421 <210> SEQ ID NO: 11
422 <211> LENGTH: 35
                             Same erro
423 <212> TYPE: DNA
424 <213> ORGANISM: (Primer
426 <400> SEQUENCE: 31
                                                                             35
427 ccttacaaag gcaaaggcat ccgttacgtt ggtga
430 <210> SEQ ID NO: 12
431 <211> LENGTH: 35
432 <212> TYPE: DNA/
433 <213> ORGANISM:\Primer
435 <400> SEQUENCE: 12
436 tcaccaacgt aacggatgcc tttgcctttg taagg
                                                                             35
439 <210> SEO ID NO: 13
440 <211> LENGTH: 30
441 <212> TYPE: DNA
                                 The type of errors shown exist throughout
                                 the Sequence Listing. Please check subsequent
                                 outperions for similar errors.
```

RAW SEQUENCE LISTING

VERIFICATION SUMMARY

DATE: 02/27/2006

PATENT APPLICATION: US/10/568,737

TIME: 15:06:54

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\02272006\J568737.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application

Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date